modulates GLUTX expression and/or activity. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant GLUTX expression or GLUTX activity in which a test sample is obtained and GLUTX nucleic acids or GLUTX polypeptides are detected (*e.g.*, wherein the presence of a particular level of GLUTX expression or a particular GLUTX allelic variant is diagnostic for a subject that can be administered an agent to treat a disorder associated with aberrant GLUTX expression or GLUTX activity).

The methods of the invention can also be used to detect genetic alterations in a GLUTX. In preferred embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic alteration characterized by at least one alteration affecting the integrity of the gene encoding a GLUTX polypeptide or the misexpression of the GLUTX gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of: (1) a deletion of one or more nucleotides from a GLUTX gene; (2) an addition of one or more nucleotides to a GLUTX gene; (3) a substitution of one or more nucleotides of a GLUTX gene; (4) a chromosomal rearrangement of a GLUTX gene; (5) an alteration in the level of a messenger RNA transcript of a GLUTX gene; (6) aberrant modification of a GLUTX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a GLUTX gene; and (10) inappropriate post-translational modification of a GLUTX polypeptide. As described herein, there are a large number of assay techniques known in the art which can be used for detecting alterations in a GLUTX gene.

In certain embodiments, detection of the alteration involves the use of a probe/primer in a polymerase chain reaction (PCR; see, *e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or alternatively, in a ligation chain reaction (LCR; see, *e.g.*, Landegran *et al.*, *Science* 241:1077-1080, 1988; and Nakazawa *et al. Proc. Natl. Acad. Sci. USA* 91:360-364, 1994), the latter of which can be particularly useful for detecting point mutations in the GLUTX gene (see Abavaya *et al.*, *Nucl. Acids Res.* 23:675-681, 1995). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic DNA, mRNA, or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a GLUTX gene under conditions such that hybridization and amplification of the GLUTX nucleic acid (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, *Proc. Natl. Acad. Sci USA* 87:1874-1878, 1990), transcriptional amplification system (Kwoh *et al.*, *Proc. Natl. Acad. Sci USA* 86:1173-1177, 1989), Q-Beta Replicase (Lizardi *et al.*, *Bio/Technology* 6:1197, 1988), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of ordinary skill in the art. These detection schemes are especially useful for the detection of nucleic acid

molecules if such molecules are present in very low number.

In an alternative embodiment, alterations in a GLUTX gene from a sample cell can be identified by identifying changes in a restriction enzyme cleavage pattern. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, *e.g.*, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, alterations in GLUTX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing tens to thousands of oligonucleotide probes (Cronin *et al.*, *Human Mutation* 7:244-255, 1996); Kozal *et al.*, *Nature Medicine* 2:753-759, 1996). For example, alterations in GLUTX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.